

SEQUENCE LISTING

<110> Li, Chuan-Yuan
 Zhang, Xiuwu
 Dewhirst, Mark W
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15	aaa tta gaa tca agt cca gag tca ctg gga ctt tct ttt acc atg ccc	1730
	Lys Leu Glu Ser Ser Pro Glu Ser Leu Gly Leu Ser Phe Thr Met Pro	
20	cag att caa gat cag cca gca agt cct tct gat gga agc act aga caa	1778
	Gln Ile Gln Asp Gln Pro Ala Ser Pro Ser Asp Gly Ser Thr Arg Gln	
25	agt tca cct gag aga ctt ctt cag gaa aac gta aac act cct aac ttt	1826
	Ser Ser Pro Glu Arg Leu Leu Gln Glu Asn Val Asn Thr Pro Asn Phe	
30	tcc cag cct aac agt ccc agt gaa tat tgc ttt gat gtg gat agc gat	1874
	Ser Gln Pro Asn Ser Pro Ser Glu Tyr Cys Phe Asp Val Asp Ser Asp	
35	atg gtc aat gta ttc aag ttg gaa ctg gtg gaa aaa ctg ttt gct gaa	1922
	Met Val Asn Val Phe Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu	
40	gac aca gag gca aag aat cca ttt tca act cag gac act gat tta gat	1970
	Asp Thr Glu Ala Lys Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp	
45	ttg gag atg ctg gct ccc tat atc cca atg gat gat gat ttc cag tta	2018
	Leu Glu Met Leu Ala Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu	
50	cgt tcc ttt gat cag ttg tca cca tta gag agc aat tct cca agc cct	2066
	Arg Ser Phe Asp Gln Leu Ser Pro Leu Glu Ser Asn Ser Pro Ser Pro	
55	cca agt atg agc aca gtt act ggg ttc cag cag acc cag tta cag aaa	2114
	Pro Ser Met Ser Thr Val Thr Gly Phe Gln Gln Thr Gln Leu Gln Lys	
60	cct acc atc act gcc act gcc acc aca act gcc acc act gat gaa tca	2162
	Pro Thr Ile Thr Ala Thr Ala Thr Thr Thr Ala Thr Thr Asp Glu Ser	
65	aaa aca gag acg aag gac aat aaa gaa gat att aaa ata ctg att gca	2210
	Lys Thr Glu Thr Lys Asp Asn Lys Glu Asp Ile Lys Ile Leu Ile Ala	
70	tct cca tct tct acc caa gta cct caa gaa acg acc act gct aag gca	2258
	Ser Pro Ser Ser Thr Gln Val Pro Gln Glu Thr Thr Thr Ala Lys Ala	
75	tca gca tac agt ggc act cac agt cgg aca gcc tca cca gac aga gca	2306
	Ser Ala Tyr Ser Gly Thr His Ser Arg Thr Ala Ser Pro Asp Arg Ala	
80	gga aag aga gtc ata gaa cag aca gac aaa gct cat cca agg agc ctt	2354
	Gly Lys Arg Val Ile Glu Gln Thr Asp Lys Ala His Pro Arg Ser Leu	

5	aag ctg tct gcc act ttg aat caa aga aat act gtt cct gag gaa gaa	2402
	Lys Leu Ser Ala Thr Leu Asn Gln Arg Asn Thr Val Pro Glu Glu Glu	
	700 705 710 715	
10	tta aac cca aag aca ata gct tcg cag aat gct cag agg aag cga aaa	2450
	Leu Asn Pro Lys Thr Ile Ala Ser Gln Asn Ala Gln Arg Lys Arg Lys	
	720 725 730	
15	atg gaa cat gat ggc tcc ctt ttt caa gca gca gga att gga aca tta	2498
	Met Glu His Asp Gly Ser Leu Phe Gln Ala Ala Gly Ile Gly Thr Leu	
	735 740 745	
20	ttg cag caa cca ggt gac tgt gca cct act atg tca ctt tcc tgg aaa	2546
	Leu Gln Gln Pro Gly Asp Cys Ala Pro Thr Met Ser Leu Ser Trp Lys	
	750 755 760	
25	cga gtg aaa gga ttc ata tct agt gaa cag aat gga acg gag caa aag	2594
	Arg Val Lys Gly Phe Ile Ser Ser Glu Gln Asn Gly Thr Glu Gln Lys	
	765 770 775	
30	act att att tta ata ccc tcc gat tta gca tgc aga ctg ctg ggg cag	2642
	Thr Ile Ile Leu Ile Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly Gln	
	780 785 790 795	
35	tca atg gat gag agt gga tta cca cag ctg acc agt tac gat tgt gaa	2690
	Ser Met Asp Glu Ser Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys Glu	
	800 805 810	
40	gtt aat gct ccc ata caa ggc agc aga aac cta ctg cag ggt gaa gaa	2738
	Val Asn Ala Pro Ile Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu Glu	
	815 820 825	
45	tta ctc aga gct ttg gat caa gtt aac tga gcgtttccta atctcattcc	2788
	Leu Leu Arg Ala Leu Asp Gln Val Asn	
	830 835	
50	ttttgattgt taatgttttt gttcagttgt tgttgtttgt tgggtttttg tttctgttgg	2848
	ttattttttgg aactggtgg ctcagcagtc tatttatatt ttctatatct aatttttagaa	2908
	gcctggctac aatactgcac aaactcagat agtttagttt tcatcccctt tctacttaat	2968
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	acaatatatt ttcttttaaaa aaccagcagt tactcatgca atatattctg catttataaa	3328
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 10 atdtttcggt cccttgctct ttgtgggttg gtctaact aactgtactg ttttggtata 3928
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25 Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys
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30 Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His
 35 40 45

35 Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile
 50 55 60

40 Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Gly Leu Asp Ser
 65 70 75 80

45 Glu Asp Glu Met Lys Ala Gln Met Asp Cys Phe Tyr Leu Lys Ala Leu
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50 Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Val Tyr Ile
 100 105 110

55 Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr
 115 120 125

60 Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met
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65 Arg Glu Met Leu Thr His Arg Asn Gly Pro Val Arg Lys Gly Lys Glu
 145 150 155 160

70 Leu Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr
 165 170 175

Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu
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 His Cys Thr Gly His Ile His Val Tyr Asp Thr Asn Ser Asn Gln Pro
 195 200 205
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 Gln Cys Gly Tyr Lys Lys Pro Pro Met Thr Cys Leu Val Leu Ile Cys
 210 215 220
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 Glu Pro Ile Pro His Pro Ser Asn Ile Glu Ile Pro Leu Asp Ser Lys
 225 230 235 240
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 Thr Phe Leu Ser Arg His Ser Leu Asp Met Lys Phe Ser Tyr Cys Asp
 245 250 255
 Glu Arg Ile Thr Glu Leu Met Gly Tyr Glu Pro Glu Glu Leu Leu Gly
 260 265 270
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 Arg Ser Ile Tyr Glu Tyr Tyr His Ala Leu Asp Ser Asp His Leu Thr
 275 280 285
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 Lys Thr His His Asp Met Phe Thr Lys Gly Gln Val Thr Thr Gly Gln
 290 295 300
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 Tyr Arg Met Leu Ala Lys Arg Gly Gly Tyr Val Trp Val Glu Thr Gln
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 Ala Thr Val Ile Tyr Asn Thr Lys Asn Ser Gln Pro Gln Cys Ile Val
 325 330 335
 Cys Val Asn Tyr Val Val Ser Gly Ile Ile Gln His Asp Leu Ile Phe
 340 345 350
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 Ser Leu Gln Gln Thr Glu Ser Val Leu Lys Pro Val Glu Ser Ser Asp
 355 360 365
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 Met Lys Met Thr Gln Leu Phe Thr Lys Val Glu Ser Glu Asp Thr Ser
 370 375 380
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 Cys Leu Phe Asp Lys Leu Lys Lys Glu Pro Asp Ala Leu Thr Leu Leu
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 Ala Pro Ala Ala Gly Asp Thr Ile Ile Ser Leu Asp Phe Gly Ser Asp
 405 410 415
 Asp Thr Glu Thr Glu Asp Gln Gln Leu Glu Asp Val Pro Leu Tyr Asn
 420 425 430

Asp Val Met Phe Pro Ser Ser Asn Glu Lys Leu Asn Ile Asn Leu Ala
 435 440 445
 5 Met Ser Pro Leu Pro Ser Ser Glu Thr Pro Lys Pro Leu Arg Ser Ser
 450 455 460
 10 Ala Asp Pro Ala Leu Asn Gln Glu Val Ala Leu Lys Leu Glu Ser Ser
 465 470 475 480
 15 Pro Glu Ser Leu Gly Leu Ser Phe Thr Met Pro Gln Ile Gln Asp Gln
 485 490 495
 20 Pro Ala Ser Pro Ser Asp Gly Ser Thr Arg Gln Ser Ser Pro Glu Arg
 500 505 510
 Leu Leu Gln Glu Asn Val Asn Thr Pro Asn Phe Ser Gln Pro Asn Ser
 515 520 525
 25 Pro Ser Glu Tyr Cys Phe Asp Val Asp Ser Asp Met Val Asn Val Phe
 530 535 540
 30 Lys Leu Glu Leu Val Glu Lys Leu Phe Ala Glu Asp Thr Glu Ala Lys
 545 550 555 560
 35 Asn Pro Phe Ser Thr Gln Asp Thr Asp Leu Asp Leu Glu Met Leu Ala
 565 570 575
 40 Pro Tyr Ile Pro Met Asp Asp Asp Phe Gln Leu Arg Ser Phe Asp Gln
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 Leu Ser Pro Leu Glu Ser Asn Ser Pro Ser Pro Pro Ser Met Ser Thr
 595 600 605
 45 Val Thr Gly Phe Gln Gln Thr Gln Leu Gln Lys Pro Thr Ile Thr Ala
 610 615 620
 50 Thr Ala Thr Thr Thr Ala Thr Thr Asp Glu Ser Lys Thr Glu Thr Lys
 625 630 635 640
 55 Asp Asn Lys Glu Asp Ile Lys Ile Leu Ile Ala Ser Pro Ser Ser Thr
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 60 Gln Val Pro Gln Glu Thr Thr Thr Ala Lys Ala Ser Ala Tyr Ser Gly
 660 665 670
 Thr His Ser Arg Thr Ala Ser Pro Asp Arg Ala Gly Lys Arg Val Ile
 675 680 685

Glu Gln Thr Asp Lys Ala His Pro Arg Ser Leu Lys Leu Ser Ala Thr
 690 695 700

5

Leu Asn Gln Arg Asn Thr Val Pro Glu Glu Glu Leu Asn Pro Lys Thr
 705 710 715 720

10

Ile Ala Ser Gln Asn Ala Gln Arg Lys Arg Lys Met Glu His Asp Gly
 725 730 735

15

Ser Leu Phe Gln Ala Ala Gly Ile Gly Thr Leu Leu Gln Gln Pro Gly
 740 745 750

20

Asp Cys Ala Pro Thr Met Ser Leu Ser Trp Lys Arg Val Lys Gly Phe
 755 760 765

Ile Ser Ser Glu Gln Asn Gly Thr Glu Gln Lys Thr Ile Ile Leu Ile
 770 775 780

25

Pro Ser Asp Leu Ala Cys Arg Leu Leu Gly Gln Ser Met Asp Glu Ser
 785 790 795 800

30

Gly Leu Pro Gln Leu Thr Ser Tyr Asp Cys Glu Val Asn Ala Pro Ile
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Gln Gly Ser Arg Asn Leu Leu Gln Gly Glu Glu Leu Leu Arg Ala Leu
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40

Asp Gln Val Asn
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 <211> 55
 <212> DNA
 <213> Artificial

50

<220>
 <221> misc_feature
 <222> (20)..(28)
 <223> n can be any nucleotide, up to 4 of which can be missing,
 55 representing a single stranded loop of from 5-9 bases, the
 hairpin loop remaining single-stranded when bases 1-19 and 29-47
 hybridize to each other to form a duplex

60

<220>
 <221> misc_feature
 <222> (48)..(55)
 <223> n can be any nucleotide, up to 6 of which can be missing,
 representing a 3' overhang of from 2-8 nucleotides, the 3'
 overhang remaining single stranded when the duplex forms between

nucleotides 1-19 and 29-47

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10 <210> 6
 <211> 53
 <212> DNA
 <213> Artificial

15 <220>
 <223> Specific sequence of an siRNA used to target human HIF-1a

20 <220>
 <221> misc_feature
 <222> (1)..(19)
 <223> Sense strand of an siRNA used to target human HIF-1a. Sequence
corresponds to bases 528-546 of Genbank Accession No. NM_001530.
This sequence forms the double stranded region of a hairpin by
intramolecular hybridization with bases 29-47.

25 <220>
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 <222> (20)..(28)
 <223> 9 base loop structure, whichs stays single stranded when bases
1-19 and 29-47 form a duplex

30 <220>
 <221> misc_feature
 <222> (29)..(47)
 <223> Antisense strand of an siRNA used to target human HIF-1a.
Sequence corresponds to the reverse complement of bases 528-546
35 of NM_001530. This sequence forms the double stranded region of
a hairpin by intramolecular hybridization with bases 1-19.

40 <220>
 <221> misc_feature
 <222> (48)..(53)
 <223> 6 base 3' overhang, which stays single stranded when bases 1-19
and 29-47 form a duplex

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50 <210> 7
 <211> 19
 <212> DNA
 <213> Homo sapiens

55 <400> 7
atgacatgaa agcacagat 19

60 <210> 8
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <223> Artificial sense strand designed with no known homology to any
human gene to be used to create a negative control siRNA

<400> 8
aattctccga acgtgtcacg t 21

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<210> 9
<211> 21
<212> DNA
10 <213> Homo sapiens

<400> 9
tcaagatcat tgctctcct g 21

15

<210> 10
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<212> DNA
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<400> 10
ctgcttgctg atccacatct g 21

25

<210> 11
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<400> 11
ctgatcatct gacaaaaact c 21

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<210> 12
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<400> 12
gtttcaaccc agacatatcc ac 22